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EXAMINER	
GOLDBERG, JEANINE ANNE	

ART UNIT	PAPER NUMBER
1634	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/567,074	SCHERER ET AL.	
	Examiner	Art Unit	
	JEANINE A. GOLDBERG	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *30 June 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-26,31,34-39 and 41-46* is/are pending in the application.

4a) Of the above claim(s) *1-3, 6-25, 34-39, 42* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *4,5,26,31,41 and 43-46* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *5/07*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. This action is in response to the papers filed June 30, 2008. Currently, claims 1-26, 31, 34-39, 41-46 are pending. Claims 1-3, 6-25, 34-39, 42 have been withdrawn as drawn to non-elected subject matter.

Election/Restrictions

2. Applicant's election with traverse of Group II, Claims 4-5, 26, 31, 41, 43-46 in the paper filed June 30, 2008 is acknowledged.

The examiner thanks applicants for pointing out that Claims 43-46 were inadvertently grouped with Group I when they should be grouped with elected Group II. Claims 43-46 are hereby placed in Group II.

Moreover, Claim 31 which depends on Claim 31 is within Group II.

The response further asserts that restriction to a single polymorphism is unduly restrictive. The response asserts that there would not be a serious search and examination burden to the Office and request reconsideration of the restriction requirement to include at least all of the variants to the EMP2B gene identified in the specification. This argument has been reviewed, but is deemed not persuasive. Current Claim 4 appears to be drawn to a generic linking claim. In the event that an allowable generic linking claims is found, the examiner will consider rejoinder of the variants encompassed within the scope of the allowable generic linking claim. However, no allowable generic or linking claim has been presented at this time.

Applicants argue that they are entitled to claim the entire genus of variations of the EPM2B gene that are associated with Lafora's disease. The response states that the members of the genus have a substantial common structure, namely the nucleic acid sequence of EPM2B, as set forth in SEQ ID NO: 1. This argument has been reviewed but is not persuasive. The "substantial common core" is known in the art, namely the "wild type" EPM2B gene is known in the art. It is the differences between the common core that applicants (i.e. the variants) are relying upon for patentability and not the common core structure that was known in the art. Thus, the variants are drawn to what is different from the common core and not the commonality of the core.

Claims 1-3, 6-25, 31, 34-39, 42 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement.

The requirement is still deemed proper and is therefore made FINAL.

This application contains claims 1-3, 6-25, 31, 34-39, 42 have drawn to an invention nonelected with traverse in the paper filed June 30, 2008. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01.

Priority

3. This application is a 371 of PCT/CA04/01449, July 30, 2004 which claims priority to 60/491,968, filed August 4, 2003.

Drawings

4. The drawings are objected to because they contain sequences which have not been identified by SEQ ID NO. Appropriate correction is required.

Sequence Rules

5. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825.

a. Pages 21 and 46 do not contain a SEQ ID NO: for identification.

b. The drawings also lack SEQ ID NO: for each of the sequences greater than 10 nucleotides in length.

Information Disclosure Statement

6. The listing of references in the specification is not a proper information disclosure statement. 37 CFR 1.98(b) requires a list of all patents, publications, or other information submitted for consideration by the Office, and MPEP § 609 A(1) states, "the

list may not be incorporated into the specification but must be submitted in a separate paper." Therefore, unless the references have been cited by the examiner on form PTO-892, they have not been considered.

c. The specification contains a list on pages 56-60 of the specification.

Claim Rejections - 35 USC § 112-Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 4, 31, 41, 43, 45, are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims broadly encompass any mutation which is a missense, nonsense or frameshift mutation in SEQ ID NO: 1 which results in a “deleterious effect” on the encoded protein product. The claims require mutations with a particular function, namely mutations which result in a deleterious effect on the encoded protein.

Vas-Cath Inc. V. Mahurkar, 19 USPQ2b 1111, clearly states that “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the ‘written description’ inquiry, whatever is now claimed”. Applicant is reminded that *Vas-*

Cath makes clear that the written description provision of 35 USC 112 is severable from its enablement provision. In *The Regents of the University of California v. Eli Lilly* (43 USPQ2b 1398-1412), the court held that a generic statement which defines a genus of nucleic acids by only their functional activity does not provide an adequate written description of the genus. The court indicated that while Applicants are not required to disclose every species encompassed by a genus, the description of a genus is achieved by the recitation of a representative number of DNA molecules, usually defined by a nucleotide sequence, falling within the scope of the claimed genus. At section B(1), the court states that "An adequate written description of a DNA…' required a precise definition, such as by structure, formula, chemical name, or physical properties', not a mere wish or plan for obtaining the claimed chemical invention".

In analyzing whether the written description requirement is met for a genus claim, it is first determined whether a representative number of species have been described by their complete structure. With respect to claims which encompass variants, as provided in Example 11 of the Written Description Guidelines, no common structural attributes identify the members of the genus. The current claims encompass a large genus of nucleic acids which comprise missense, nonsense or frameshift mutations in SEQ ID NO: 1 which results in a deleterious effect on the encoded protein product. The genus includes an enormous number of mutations for which no written description is provided in the specification. The specification teaches 21 particularly named mutations (see page 56). However, it is unclear from the specification whether these mutations in SEQ ID NO: 1 are deleterious on the encoded protein product. The specification does

not provide any description of which mutations have a deleterious effect on the encoded protein. The art teaches that additional mutations have been found (see Ianzano et al. Human Mutation Database in Brief #847, http://projects.tcag.ca/lafora). In the database, of mutations of NHLRC1 (EPM2B), 51 mutations have been indexed. The database classifies several missense mutations as mutations and not associated with disease. Moreover, Lohi et al. (Neurology, Vol. 68, pages 996-1001, 2007) teaches hidden and novel Lafora disease gene mutations and likely coding mutations. The Table notes that several of the mutations cause protein truncations or no protein is made, but 7 mutations are not taught to cause any deleterious effect on the encoded protein (see page 1000).

With respect to the claims which encompass dog or canine mutations, the specification further states that Lafora's disease has also been discovered in dogs with surprising frequency. The specification analyzes a single breed of dogs, namely the miniature wirehaired dachshund (MWHD) (page 48). A repeat expansion is analyzed. The specification teaches all affected animals had bi-alleleic expansions of dodecamer repeat (page 51). This single expansion mutation is not within the scope of the claims, as it is not a missense, nonsense or framentshit muftation. Thus, the specification and the art have not taught any mutations within the scope of the instant claims in dogs which have a deleterious effect on the encoded protein.

The general knowledge and level of skill in the art do not supplement the omitted description because specific, not general guidance is what is needed. Since the

disclosure fails to describe the common attributes or characteristics that identify members of the genus, and because the genus is highly variant, mutations of SEQ ID NO: 1 which cause a deleterious effect on the encoded protein alone is insufficient to describe the genus. There is no description of the mutational sites that exist in nature and there is no description of how the structure of SEQ ID NO: 1, namely EPM2B/NHLRC1, relates to the structure of any mutations which do not cause a deleterious effect on the encoded protein. The general knowledge in the art concerning mutations does not provide any indication of how the structure of one allele is representative of unknown alleles. The nature of alleles is such that they are variant structures, and in the present state of the art the structure of one does not provide guidance to the structure of others. The common attributes are not described. The specification provides no correlation between structure of mutations and the function of such mutations. The mutations shown are not representative of the genus of any mutation associated with Lafora's disease because it is not clear which mutations within the gene (coding or non-coding) region of Lafora nucleic acid would have the same effect. One of skill in the art would conclude that applicant was not in possession of the claimed genus because a description of only one member of this genus is not representative of the variants of the genus and is insufficient to support the claim. Accordingly, Applicants have not adequately disclosed the relevant identifying characteristics of a representative number of species within the claimed genus.

Claim Rejections - 35 USC § 112- Enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

8. Claims 4-5, 26, 31, 41, 43-46 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for

A method of detecting Lafora's disease in a human subject comprising obtaining a sample from the human subject and

detecting a G at position 205 of SEQ ID NO: 1

wherein the presence of a G at position 205 of SEQ ID NO: 1 is indicative of Lafora's disease,

does not reasonably provide enablement for a method of detecting Lafora's disease in a mammal, including a human, by detecting a missense, nonsense or frameshift which results in a deleterious effect on the encoded protein product including a nucleotide change at position 205 of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

9. Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 8 USPQ2d 1400 (CA FC 1988). *Wands* states at page 1404,

> "Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in Ex parte Forman.

> They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims."

The nature of the invention and breadth of claims

Claims 4-5, 26, 31, 45 are drawn to a method of detecting Lafora's disease in a mammal, including a human, by detecting a missense, nonsense or frameshift which results in a deleterious effect on the encoded protein product including a nucleotide change at position 205 of SEQ ID NO: 1.

Claim 41 is drawn to a method of detecting the presence of Lafora's disease in a human comprising detecting a mutation in the EPM2B gene nucleic acid sequence.

Claim 43 is drawn to a method of detecting the presence or absence of a mutation in the EPM2B gene by comparing the test sample to a nucleic acid sequence set forth in SEQ ID NO: 1 and determining the differences. The claim broadly encompasses any test sample.

Claims 44 , 46 are drawn to a method for diagnosing the presence or predisposition to Lafora's disease by analyzing a nucleic acid sample from a human to determine the presence of a EPM2B gene mutation listed in Table 1 wherein the presence of an EPM2B gene mutation indicates the individual has or is at risk for development of Lafora's disease.

The invention is in a class of invention which the CAFC has characterized as "the unpredictable arts such as chemistry and biology." Mycogen Plant Sci., Inc. v. Monsanto Co., 243 F.3d 1316, 1330 (Fed. Cir. 2001).

The unpredictability of the art and the state of the prior art

The art teaches genetic mapping of a new Lafora progressive myoclonus epilepsy locus (EPM2B) on 6p22. Chan et al. (J. Med. Genet. Vol. 40, pages 671-675, 2003) states they have identified a second LD gene locus named EPM2B at 6q22 based on a study of LD families from a F-C isolated. Chan teaches a nine marker haplotype is identical and homozygous in all patients (page 874, col. 1).

Chan et al. (Nature Genetics, Vol. 35, No. 2, pages 125-127, September 2003) teaches mutations in NHLRC1 cause progressive myoclonus epilepsy. NHLRC1 is also called PEM2B. Chan teaches the identification of 17 different DNA sequence alterations in 26 families which were not present in 100 control chromosomes (Page 125, col.2). Table 1 illustrates a summary of mutations associated with Lafora disease. Chan teaches the C205G nucleotide chance is P69A which causes a missense RING finger, however provides no information whether this alteration causes a deleterious effect on the protein product.

Ianzano et al. (Human Mutation database in Brief #847, 2005) teaches Lafora progressive myoclonus epilepsy mutation database-EPM2A and HNLRC1 (EMP2B) genes. The database for Lafora progressive myoclonus epilepsy mutation and polymorphisms is accessible at http://projects.tcag.ca/lafora. On August 22, 2008 the data base was accessed and there are 51 entries for EPM2B/NHLRC1.

Singh et al. (J. Med Genetics, Vol. 43, e48, 2006) teaches novel NHLRC1 mutations and genotype-phenotype correlations in patients with Lafora's progressive myoclonic epilepsy. Singh teaches identification of 5 new mutations. Figure 1 provides a representation of 39 mutations in the NHLRC1 gene and the frequency. P69A appears to be the most frequent mutation found.

Lohi et al. (Neurology, Vol. 68, pages 996-1001, 2007) teaches a heterozygous deletion of the entire EPM2B gene and seven new mutations. Table 1 illustrates

mutations which are missense, but no analysis of the effect on the protein has been provided. Moreover, the table notes one variant as a SNP rather than a mutation.

The level of unpredictability in associating any particular allele with a specific phenotype is even higher. The high level of unpredictability is demonstrated by the prior art, the post filing art, and the instant specification. There is a large body of knowledge in the prior art related to polymorphisms in general, and their association with diseases. However, the art is highly unpredictable with regard to the functionality of polymorphic sites in genomic DNA. After a screening assay identifies polymorphisms, it is unpredictable whether any such polymorphisms would be associated with any phenotypic trait, such as a disease state.

Lucentini (The Scientist; 2004, vol 24, page 20) teaches that most gene association studies are typically wrong. Lucentini teaches that it is strikingly common for follow-up studies to find gene-disease associations wrong (left column, 3rd paragraph). Lucentini teaches that two recent studies found that typically when a finding is first published linking a given gene to a disease there is only roughly a one-third chance that the study will reliably confirm the finding (left column, 3rd paragraph). Lucentini teaches that bigger sample sizes and more family-based studies, along with revising statistical methods, should be included in the gene association studies (middle column, 1 st complete paragraph). In the instant case, the specification only provides information that the variants within EPM2B exist, but provides no guidance that it has any effect on the EPM2B gene, expression, or activity, let alone any potential diagnostic effect.

The art teaches genetic variations and associations are often irreproducible. Hirschhorn et al. (Genetics in Medicine. Vol. 4, No. 2, pages 45-61, March 2002) teaches that most reported associations are not robust. Of the 166 associations studied three or more times, only 6 have been consistently replicated. Hirschhorn *et al.* suggest

a number of reasons for the irreproducibility of studies, suggesting population stratification, linkage disequilibrium, gene-gene or gene-environment interactions, and weak genetic effects and lack of power are possible factors that lead to such irreproducibility. Hirschhorn *et al.* caution that the current irreproducibility of most association studies should raise a cautionary alarm when considering their use as diagnostics and prognostics (p. 60, Col. 2). Thus, Hirschhorn cautions in drawing conclusions from a single report of an association between a genetic variant and disease susceptibility.

Additionally, Ioannidis (Nature Genetics, Vol. 29, pages 306-309, November 2001) teaches that the results of the first study correlate only modestly with subsequent research on the same association (abstract). Ioannidis teaches that both bias and genuine population diversity might explain why early association studies tend to overestimate the disease protection or predisposition conferred by a genetic polymorphism (abstract).

The art teaches that presence of SNPs in the same gene does not indicate that each of the genes is associated with the same diseases. Meyer et al. (PG Pub 2003/0092019), for example, teaches that SNPs in the CADPKL gene are not each associated with neuropsychiatric disorders such as schizophrenia. Specifically Meyer teaches that cadpkl5 and cadpkl6 are not associated with the disease, however cadpkl7 has a p-value of less than 0.05, therefore an association exists. Each of these polymorphisms are SNPs within the CADPKL gene, however, it is apparent that they are not all associated in the same manner with disease. Thus, Meyer exemplifies that the association of a single SNP in a gene does not indicate that all SNPs within the gene are associated with the disease.

Guidance in the Specification.

The specification provides no evidence that all missense, nonsense, or frameshift mutations in SEQ ID NO: 1 cause a deleterious effect on the encoded protein or are associated with Lafora's disease.

The specification teaches 17 different DNA sequence alterations are described in EPM2B in 26 families including 8 deletions and 1 insertion leading to frame-shifts, 7 missense, and 1 non-sense change (Table 1). These mutations were found in families in both homozygous (18) and compound heterozygous (8) recessive states. The most common mutation identified (7 families) was a homozygous 205C.fwdarw.G transition resulting in a proline to alanine change in the RING-finger domain.

All of the mutations detected would affect the putative RING or NHL motifs, or would be predicted to lead to a frame-shift or cause drastic structural change in the protein (LD483 carries a 260T.fwdarw.C nucleotide change which would lead to a leucine to proline alteration).

Four silent DNA sequence-coding variants were identified. Three of them T312C (H104H), G372C (G124G) and T1020C (G340G) were present in five, two, and one of 100 control chromosomes, respectively. The most common polymorphism detected, C332T (P111L) (FIG. 1) was observed on 42 of 100 control chromosomes.

The guidance provided by the specification amounts to an invitation for the skilled artisan to try and follow the disclosed instructions to make and use the claimed invention.

Quantity of Experimentation

The quantity of experimentation in this area is extremely large since there is significant number of parameters which would have to be studied to enable the skilled artisan to practice the claimed invention as broadly as claimed.

The claims are drawn to detecting Lafora's disease in any mammal. Claim 31, 41, 44 are drawn specifically to humans. The specification teaches 17 different DNA alterations in EPM2B in 26 human families (see Table 1). The specification further states that Lafora's disease has also been discovered in dogs with surprising frequency. The specification analyzes a single breed of dogs, namely the miniature wirehaired dachshund (MWHD) (page 48). A repeat expansion is analyzed. The specification teaches all affected animals had bi-allelic expansions of dodecamer repeat (page 51). This single expansion mutation is not within the scope of the claims, as it is not a missense, nonsense or frameshift mutation. Thus, the specification and the art have not taught any mutations within the scope of the instant claims in dogs which have a deleterious effect on the encoded protein. While the skilled artisan could perform additional undue experimentation to determine if there are missense, nonsense or frameshift mutations that results in a deleterious effect on the encoded protein, such experimentation is unpredictable and undue. There is no analysis in the specification or the art regarding cats, monkeys, rabbits and mutations that may exist and whether these mutations may have any association with Lafora's disease.

The claims are broadly drawn to detecting Lafora's disease by detecting Lafora's disease by detecting any missense, nonsense or frameshift mutation which has a deleterious effect on the encoded protein product. The claims appear to state that the presence of any missense, nonsense or frameshift which has a deleterious effect on the encoded protein product is indicative of Lafora's disease. This logic does not appear to be supported by the evidence of record. The specification teaches P111L is present in

42/100 control chromosomes. Thus, it is unpredictable which missense, nonsense or frameshift within SEQ ID NO: 1, have a deleterious effect on the encoded protein product. Further it is unpredictable which missense, nonsense or frameshift which has a deleterious effect on the encoded protein product are indicative of Lafora's disease. At the time the invention was made, the specification taught 17 variations within 26 families. One of these variations was found in a high percentage of control chromosomes. It would have been unpredictable at the time the invention as made to determine and know which variations of SEQ ID NO: 1 are associated with Lafora's disease absent further unpredictable and undue experimentation. While the skilled artisan could assay for additional mutations, it would have been unpredictable which mutations result in a deleterious effect on the encoded protein product and further which variations are indicative or diagnostic of Lafora's disease.

This would require significant inventive effort, with each of the many intervening steps, upon effective reduction to practice, not providing any guarantee of success in the succeeding steps.

Level of Skill in the Art

The level of skill in the art is deemed to be high.

Conclusion

In the instant case, as discussed above, in a highly unpredictable art where the association of mutations and diseases has not been established it is unpredictable the skilled artisan could practice the claimed invention as broadly as claimed. The prior art and the specification provides insufficient guidance to overcome the art recognized difficulties of association studies. Thus given the broad claims in an art whose nature is

identified as unpredictable, the unpredictability of that art, the large quantity of research required to define these unpredictable variables, the lack of guidance provided in the specification, the absence of a working example and the negative teachings in the prior art balanced only against the high skill level in the art, it is the position of the examiner that it would require undue experimentation for one of skill in the art to perform the method of the claim as broadly written.

Claim Rejections - 35 USC § 112- Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

10. Claims4-5, 26, 31, 41, 45 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claims 4-5, 26, 31, 45 are indefinite because it is unclear what is required by the instant methods. The claims are drawn to a method of detecting Lafora's disease however the final method step is drawn to detecting a missense, nonsense or frameshift mutation. It is unclear whether the claims are drawn to detecting Lafora's disease or merely detecting a mutation in SEQ ID NO: 1.

B) Claim 41 is indefinite because it is unclear what is required by the instant methods. The claims are drawn to a method of detecting Lafora's disease however the final method step is drawn to detecting a mutation. It is unclear whether the claims are drawn to detecting Lafora's disease or merely detecting a mutation.

C) Claim 41 is indefinite over the recitation “substantial sequence homology”. The term "substantial" in claim 41 is a relative term which renders the claim indefinite. The term "substantial" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention.

Conclusion

11. No claims allowable.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jeanine Goldberg whose telephone number is (571) 272-0743. The examiner can normally be reached Monday-Friday from 7:00 a.m. to 4:00 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner’s supervisor, Ram Shukla, can be reached on (571) 272-0735.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

The Central Fax Number for official correspondence is (571) 273-8300.

/Jeanine Goldberg/
Primary Examiner
September 29, 2008